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#9/52 UP1633

2/4-02 PCT

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RAW SEQUENCE LISTING   DATE: 05/29/2001
PATENT APPLICATION: US/09/700,354A   TIME: 16:13:36

Input Set : A:\SeqList for IRVN-007CIP2.txt
Output Set: C:\CRF3\05292001\I700354A.raw

SEQUENCE LISTING

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 5 (1) GENERAL INFORMATION:
 7       (i) APPLICANT: Gatanaga, Tetsuya
 8                      Granger, Gale A.
10      (ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
11                               Factor Receptor Releasing Enzyme Activity.
13     (iii) NUMBER OF SEQUENCES: 154
15      (iv) CORRESPONDENCE ADDRESS:
16           (A) ADDRESSEE: BOZICEVIC, FIELD, & FRANCIS, LLP
17           (B) STREET: 200 MIDDLEFIELD ROAD, #200
18           (C) CITY: Menlo Park
19           (D) STATE: CA
20           (E) COUNTRY: USA
21           (F) ZIP: 94025
23       (v) COMPUTER READABLE FORM:
24           (A) MEDIUM TYPE: Diskette
25           (B) COMPUTER: IBM Compatible
26           (C) OPERATING SYSTEM: Windows
27           (D) SOFTWARE: FastSEQ for Windows Version 2.0b
29      (vi) CURRENT APPLICATION DATA:
C--> 30           (A) APPLICATION NUMBER: US/09/700,354A
C--> 31           (B) FILING DATE: 17-Apr-2001
32           (C) CLASSIFICATION:
34     (vii) PRIOR APPLICATION DATA:
35           (A) APPLICATION NUMBER: 09/081,385
36           (B) FILING DATE: 14-MAY-1998
38           (A) APPLICATION NUMBER: PCT/US99/10793
39           (B) FILING DATE: 14-MAY-1999
42    (viii) ATTORNEY/AGENT INFORMATION:
43           (A) NAME: Francis, Carol L.
44           (B) REGISTRATION NUMBER: 36,513
45           (C) REFERENCE/DOCKET NUMBER: IRVN-007CIP2
47      (ix) TELECOMMUNICATION INFORMATION:
48           (A) TELEPHONE: 650-327-3400
49           (B) TELEFAX: 650-327-3231
50           (C) TELEX:
53 (2) INFORMATION FOR SEQ ID NO: 1:
55       (i) SEQUENCE CHARACTERISTICS:
56           (A) LENGTH: 4047 base pairs
57           (B) TYPE: nucleic acid
58           (C) STRANDEDNESS: double
59           (D) TOPOLOGY: linear
61      (ii) MOLECULE TYPE: Genomic DNA
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
65  AAGCTTTTTG CTTTCCTTCC CCGGGAAAGG CCGGGGCCAG AGACCCGCAC TCGGACCAGG      60
66  CGGGGGCTGC GGGGCCAGAG TGGGCTGGGG AGGGCTGGGA GGGCGTCTGG GGCCGGCTCC     120
67  TCCAGGCTGG GGGCCGCCAG CTCCGGGAAG GCAGTCCTGG CCTGCGGATG GGGCCGCGCG     180
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 68   TGGGGCCCGG CGGGGCGGCC TCGGGAGGCG TCCAGGCTGC GGGAGCGGGA GGAGCGGCCG     240
 69   TGCGGGCGCC AGCGCCGTGG GTGGAGGTCG CCGTCCCTCC TGAGGGGCAG CCAGTGCGTT     300
 70   TGGGACCCGG GAGCAGAGCC CGCGCCTCCC CAGCGGCCTC CCCGGGGGTC TCACCGGGTC     360
 71   ACCCGAGAGC GGAGGCCCCG GCTCCGCAGA AACCCGGGGC GGCCGCGGGG AAGCAGCGCC     420
 72   CTCAGGCGTC GGAGGAGCCC CCAGAAGGAC CTCGCGCCTT CCCGCCGGGC TCCGACCGCC     480
 73   TGGGTTCGGT GCGGGACGGC CCAGGCCGCC AGGACCCCCA AGCGCAGCTC AGTCTGCGGG     540
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 76   CAGGGAGGTG AGGGGGCTCT GTGAGCAGAG GGGGCCCCGG TGGAGAAGGC GCTGCTAGCC     720
 77   AGGGGCGGGG CAGGAGCCCA GGTGGGGACT TAAGGGTGGC TGAAGGGACC CTCAGGCTGC     780
 78   AGGGATAGGG AGGGAAGCTA GGGGTGTGGC TTGGGGAGGT GCTGGGGGAC CGCGGGCGCC     840
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 83   CCTTTCACGG AGAAAGTGTG GGCAGAAGCC AGCTCTAAAG CCCAGGCTGC CCAGCCTGCA    1140
 84   CTGGCAGAGC TGACGGAAGG CCAGGGCAGA GCCTTCCCTC CCTGTCACAG ACATGAGCCC    1200
 85   TGGAGATCTG GAATGAGGCA GATGTGCCCA GGGAAAGCTG ATCCGCCCCG ACCCAGGGCC    1260
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 88   GAGGTGATGA CTGCCTTCCA GGGGCCTGGC TGGCTGACAC TTTGCATGGC TCCTGGAGAA    1440
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 90   GCCCGGCTGG GGTGAGAAGG GGCTGGAGAC AGGTTCCTGC CAGTTCAGCC TCTAACCGGT    1560
 91   GGTCTTCATG CCTAGGAACC CACTGGGGGC TTATGAAACT GCAGGTGGCT GAGTCCTTGC    1620
 92   CATGGGGTCT CTCCTTCAGG AGGTCTGGGT GGGGCCGGAG ACTGTACCCC ACAAAGGGTC    1680
 93   CCAGGTGAGG CGGATGTGGC CTGGCGCTGT GTGGCTCTGG ACCTAGTCCT TGGGCTTGGG    1740
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 97   CAGGGAGACT CAAGTGGAAA GCCCTCATCC TTGTCCTCCA GGAGACAGGA AAACCTATGG    1980
 98   TTACAATTCC AGGGACAAGA GCGATGCATG TGAGGTGTGG CAAATCTCAC TGTTCAACTG    2040
 99   GAGAAATCAG AGACAGCTTC CTGGAGGCAG TGACACCTGG ACAGGCTTCT CCACAGGAGG    2100
100   AAGCGAGTGA GAGAAGCCAA CTGGGATGGA CCCATCATGT AGGGGGAACA GTGCGCGCAG    2160
101   AACCAACAAC CACCCCCACC CTAGGCCCAG AGCTCACGGA GAGAGCTGGG CCTCTCGGGG    2220
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103   CTATGCCTGT TCCAGGCTGC ACCAAGGTTT TGTGACTATT GGTCTGGGGT TGTTTTGCAG    2340
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106   GTGTTTTTGA AGTCTGTCCT GGGTACTGCA CATTAAAAGG AATATCATTT TCTGAAACAT    2520
107   TGCTATTTTC CACACCAGAA ATCATATCCT CTTGCTGGTC CATGTCTGAA GACCTTACAC    2580
108   GAGAAAGTCT TAATGTAAGT TTAGTAGAGT CCTTGGATGG AGAACTAATT ATATCATACA    2640
109   TTGCCGCTTT CTCACTCTGC TCTTTTTCAT CCTTGCCTAA TTTCATTTTC TTCTGCTTCT    2700
110   TTTGTTTTCT TTCTGGAGAA TCTAGCAAGA TATCTGGTGG AACATCTCGA GGTGATGAAC    2760
111   AAGGTAGAGA CTGAGATTGT AGGATTAAAG GTGGTCTTGA GCCTTTAGGA GTTCCTTCAC    2820
112   TTCCAGCAGG GGAGCATACT GGCTGTGGAG ATCTCAAGGG AAAAGATGCA GCATTCCTCA    2880
113   TTGTTGAAGA ATCTCCATCG TCACTACTTA GCCTGTGCAC CATGTGTAGG TAGTCCTCAC    2940
114   TTGAACCATG TCTAGGATTA TCAGCATGAT GATTAGCTGA ATTGCCAGAC AACGGACCAG    3000
115   AAACTTTATT ATCATGTATG TTTCTCAAAC CACCTGCAAC AATGGGACTT GATACCGATG    3060
116   CTTGTTGCAT CTGTGGATGT GTTGTGTAAC TTGAAGGATG GGAATATGGC ATGTATCCTG    3120
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117  CAGGGCTTTG TGGGGCGTAT GGACTAGGCA CTGGGCTATT TTGCTGTGGC ATAAATCTGT  3180
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119  GTTGATAATT GGAAGATGCA GGACTACTGT GCATGGAATT CTGAGAAAGT TTATACTGAG  3300
120  ACATCATCAT TCCACTTTGT ACATATCTGT TCTGCATGCT TTTCTCCCTG AAAACATTAG  3360
121  GACTCCTTGC CAGGACGGCC TGCAACAAGA CTGGTATGTC ACCTTCTGGG TCATCACTGC  3420
122  CAAGGTTATC TTTCAACTCT ATGTGATCTG TTGATACCTG GTTGAGGCTA TGGACAAGCT  3480
123  GTGAAACCAA ATTGTCATCC CTACAAGCCA AAAGGCAGTT CACCTCTTCT GCTATTCGTG  3540
124  CATTAAAGAG AAGGCTCTTT GTAGTTGTAG CAGGTAAAGG AGATGGAAGA GGCAGCTGGT  3600
125  TCAGGAGGTC TGTGAGACTA GCAATCCCCG CAAGAGTAGT AATGGGGACA TGGGGCATAT  3660
126  CCCCATTCAT CCTGAATTTC TGGAATGGTG TTGCCTATAA AAGTACTTAG TTCAGGTGCC  3720
127  AGCTGTCATT ACTTCCCATT TCCCAAACAC TGGGCGAATC GGCGTCTGAA TCCAAGGGGA  3780
128  GGCCGAGGCC GCTGTGGCGA GAGACTATAA TCCGGGCCGG GAGGGGGGGC GGCTACGGCT  3840
129  CCTCTTCCGT CTCCTCAGTG CGGGGAACAT GTAGAGCCGG GGGGAGACCA GCCGAGAAGA  3900
130  CAAATCGTTG CTTCTTCTTC CTCCTCCTCC TCCTTCTCCC ACATAGAAAC ACTCACAAAC  3960
131  ACCCGACCAC GGGCCCGAGC TACCGGGGGG GCATCGCCGC GGGCCCGGGA ACCAATTCTC  4020
132  CTGTCGGCGG GGGCGTCCTT TGGATCC                                      4047
134  (2) INFORMATION FOR SEQ ID NO: 2:
136       (i) SEQUENCE CHARACTERISTICS:
137           (A) LENGTH: 739 base pairs
138           (B) TYPE: nucleic acid
139           (C) STRANDEDNESS: double
140           (D) TOPOLOGY: linear
142      (ii) MOLECULE TYPE: Genomic DNA
144      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
146  GGATCCAAAG GTCAAACTCC CCACCTGGCA CTGTCCCCGG AGCGGGTCGC GCCCGGCCGG   60
147  CGCGCGGCCG GGCGCTTGGC GCCAGAAGCG AGAGCCCCTC GGGGCTCGCC CCCCCGCCTC  120
148  ACCGGGTCAG TGAAAAAACG ATCAGAGTAG TGGTATTTCA CCGGCGGCCC GCAGGGCCGG  180
149  CGGACCCCGC CCCGGGCCCC TCGCGGGGAC ACCGGGGGGG CGCCGGGGGC CTCCCACTTA  240
150  TTCTACACCT CTCATGTCTC TTCACCGTGC CAGACTAGAG TCAAGCTCAA CAGGGTCTTC  300
151  TTTCCCCGCT GATTCCGCCA AGCCCGTTCC CTTGGCTGTG GTTTCGCTGG ATAGTAGGTA  360
152  GGGACAGTGG GAATCTCGTT CATCCATTCA TGCGCGTCAC TAATTAGATG ACGAGGCATT  420
153  TGGCTACCTT AAGAGAGTCA TAGTTACTCC CGCCGTTTAC CCGCGCTTCA TTGAATTTCT  480
154  TCACTTTGAC ATTCAGAGCA CTGGGCAGAA ATCACATCGC GTCAACACCC GCCGCGGGCC  540
155  TTCGCGATGC TTTGTTTTAA TTAAACAGTC GGATTCCCCT GGTCCGCACC AGTTCTAAGT  600
156  CGGCTGCTAG GCGCCGGCCG AAGCGAGGCG CCGCGCGGAA CCGCGGCCCC CGGGGCGGAC  660
157  CCGCGGGGGG GACCGGGCCG CGGCCCCTCC GCCGCCTGCC GCCGCCGCCG CCGCCGCGCG  720
158  CCGAAGAAGA AGGGGGAAA                                               739
160  (2) INFORMATION FOR SEQ ID NO: 3:
162       (i) SEQUENCE CHARACTERISTICS:
163           (A) LENGTH: 233 base pairs
164           (B) TYPE: nucleic acid
165·          (C) STRANDEDNESS: double
166           (D) TOPOLOGY: linear
168      (ii) MOLECULE TYPE: Genomic DNA
170      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
172  CAAGAGTGGC GGCCGCAGCA GGCCCCCCGG GTGCCCGGGC CCCCCTCGAG GGGGACAGTG   60
173  CCCCCGCCGC GGGGGCCCCG CGGCGGGCCG CCGCCGGCCC CTGCCGCCCC GACCCTTCTC  120
174  CCCCCGCCGC CGCCCCCACG CGGCGCTCCC CCGGGGAGGG GGGAGGACGG GGAGCGGGGG  180
175  AGAGAGAGAG AGAGAGAGGG CGCGGGGTGG CTCGTGCCGA ATTCAAAAAG CTT         233
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179       (i) SEQUENCE CHARACTERISTICS:
180             (A) LENGTH: 2998 base pairs
181             (B) TYPE: nucleic acid
182             (C) STRANDEDNESS: double
183             (D) TOPOLOGY: linear
185      (ii) MOLECULE TYPE: Genomic DNA
187      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
189 GGATCCAAAG AATTCGGCAC GAGGTAGTCA CGGCTCTTGT CATTGTTGTA CTTGACGTTG     60
190 AGGCTGGTGA GCTTGGAAAA GTCGATGCGC AGCGTGCAGC AGGCGTTGTA GATGTTCTGC    120
191 CCGTCCAGCG ACAGCTTGGC GTGCTGGGCG CTCACGGGGT CCGCATACTG CAGCAGGGCC    180
192 TGGAACTGGT TGTTCTTGGT GAAGGTGATG ATCTTCAACA CTGTGCCGAA CTTGGAGAAA    240
193 ATCTGGTGCA GCACATCCAG GGTCACAGGG TAGAAGAGGT TCTCCACGAT GATCCTGAGC    300
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196 TTGGGAGAGC TGTCGGTCTT CAGCTCCTTG TGGTTGGAGA ACTGGATGTA GATGGGCTGG    480
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198 GTGTTCATCT CGATGAAGGC CTGGTTTTTC CCCTTCAGCA TCAGGAGGTT GGTGACCTTC    600
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202 CAAGTAGAGA AAAGCTCGTC AGATCCCCGC TTTGTACCAA CGGCTATATC TGGGACAATG    840
203 CCGTCCATGG CACACAGAGC AGACCCGCGG GGGACGGAGT GGAGGCGCCG GAATCCTGGA    900
204 GCTAGAGCTG CAGATTGAGT TGCTGCGTGA GACGAAGCGC AAGTATGAGA GTGTCCTGCA    960
205 GCTGGGCCGG GCACTGACAG CCCACCTCTA CAGCCTGCTG CAGACCCAGC ATGCACTGGG   1020
206 TGATGCCTTT GCTGACCTCA GCCAGAAGTC CCCAGAGCTT CAGGAGGAAT TTGGCTACAA   1080
207 TGCAGAGACA CAGAAACTAC TATGCAAGAA TGGGGAAACG CTGCTAGGAG CCGTGAACTT   1140
208 CTTTGTCTCT AGCATCAACA CATTGGTCAC CAAGACCATG AAGACACGC TCATGACTGT    1200
209 GAAACAGTAT GAGGCTGCCA GGCTGGAATA TGATGCCTAC CGAACAGACT TAGAGGAGCT   1260
210 GAGTCTAGGC CCCCGGGATG CAGGGACACG TGGTCGACTT GAGAGTGCCC AGGCCACTTT   1320
211 CCAGGCCCAT CGGGACAAGT ATGAGAAGCT GCGGGGAGAT GTGGCCATCA AGCTCAAGTT   1380
212 CCTGGAAGAA AACAAGATCA AGGTGATGCA CAAGCAGCTG CTGCTCTTCC ACAATGCTGT   1440
213 GTCCGCCTAC TTTGCTGGGA ACCAGAAACA GCTGGAGCAG ACCCTGCAGC AGTTCAACAT   1500
214 CAAGCTGCGG CCTCCAGGAG CTGAGAAACC CTCCTGGCTA GAGGAGCAGT GAGCTGCTCC   1560
215 CAGCCCAACT TGGCTATCAA GAAAGACATT GGGAAGGGCA GCCCCAGGGT GTGGGAGATT   1620
216 GGACATGGTA CATCCTTTGT CACTTGCCCT CTGGCTTGGG CTCCTTTTTC TGGCTGGGGC   1680
217 CTGACACCAG TTTTGCCCAC ATTGCTATGG TGGGAAGAGG GCCTGGAGGC CCAGAAGTTG   1740
218 CTGCCCTGTC TATCTTCCTG GCCACAGGGC TTCATTCCCA GATCTTTTCC TTCCACTTCA   1800
219 CAGCCAACGG CTATGACAAA ACCACTCCCT GGCCAATGGC ATCACTCTTC AGGCTGGGGT   1860
220 GTGCTCCCTG ACCAATGACA GAGCCTGAAA ATGCCCTGTC AGCCAATGGC AGCTCTTCTC   1920
221 GGACTCCCCT GGGCCAATGA TGTTGCGTCT AATACCCTTT GTCTCTCCTC TATGCGTGCC   1980
222 CATTGCAGAG AAGGGGACTG GGACCAAAGG GGTGGGGATA ATGGGGAGCC CCATTGCTGG   2040
223 CCTTGCATCT GAATAGGCCT ACCCTCACCA TTTATTCACT AATACATTTT ATTTGTGTTC   2100
224 TCTAATTTAA AATTACCTTT TCATCTTGCT TGATTTTCCT TCAGCTAAAT TAGAAATTTG   2160
225 TAGTTTTTCC CCTAAAAAAT TCAATGGCAT TCTTTCTTAT AAATTACATT CTCTGATTTT   2220
226 CTTGTCAGCC TGCTTCAAGG AAATCCATGT GTTCAAAATG CTTGCTCGCA GTTTGCTCCA   2280
227 TACCAAATGG TTGCTTAACC CAAATATCTG AGCAGCAAAT TGAGCTGATC CTTCTGGAGA   2340
228 AAGTACGGTT GAACAGCCAA GACCACTGGG TAGTCGAAGA GAAGACCACA CATCCTGAAC   2400
229 TCCCCAGTCT GGTGTGAGGG GAGGACAGCT GATAACTGGA TATGCAGTGT TCCCAGACAT   2460
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232  TCGAAGTTCA CATGGAATGC CAAAATTTCC ACAGGCCTTC TTGATTTTTT CACAGTGACC  2640
233  AAGATCAGAA GTAGAGCCCA TCAACACTAC AACCCTGCAC TGACTTTCTG ATTTCAAAAG  2700
234  CAACTCTACT CTCTCTGCAA CCCACTCAAA GTTTTTCTTT ACCATTTGGA GCCCTTCAGG  2760
235  AGTTACTTCT TTGAGGTCCC GATAAGACTG TTTGTCTTTC TGTTGGCTTC GATCTCCTGA  2820
236  TGGCCAGAGT CTCCAGGAAT CATTGTCAAT AACATCAGCA AGAACAATTT CTTTGGTGGT  2880
237  TACATCAACA CCAAATTCAA TCTTCATATC AACCAGTGTA CAATTCTGGG GCAACCAGGA  2940
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240  (2) INFORMATION FOR SEQ ID NO: 5:
242       (i) SEQUENCE CHARACTERISTICS:
243           (A) LENGTH: 4152 base pairs
244           (B) TYPE: nucleic acid
245           (C) STRANDEDNESS: double
246           (D) TOPOLOGY: linear
248      (ii) MOLECULE TYPE: Genomic DNA
250      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
252  AAGCTTTTTG TGAAAACCCT AGGATATGTC CCCTCCCTCA CCACACCCAA CCCCCCGCCC    60
253  CTGCCCCAGG ACATGACGAT GCCTCACACA CACACACACA CACACATACA CACAAGGCCG   120
254  TGAGCTGCAC GCAGGAACAT GGGCTGCACT CACGACAACA TTGAAAAAAT ATACATTATA   180
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256  CGGAGGAGGG GCCGGGGCTG CAGGACCTCA GGACTGCAAG GGCAGGAAGG GAAACAGGAC   300
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263  GAGGGATGGG GGGCCGGGGG AGGGGCAGGG CGGACTCCAG AGGGCCCGCT GGGGTTTTGA   720
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283  ACTCTTCGCT GAAGCACTTG ACAGCAGTGG TGAGGCGCAG GGGCCTGACG CCGGGCGTGG  1920
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L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:3225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:154